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<110> Gurney, Mark E.

Li, Jinhe

Pauley, Adele M.

Pharmacia & Upjohn Company

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<141> 1997-12-19

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<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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<213> Homo sapiens

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Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys
35 40 45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr
50 55 60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr
65 70 75 80

D2

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser
85 90 95

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu
100 105 110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr
115 120 125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg
130 135 140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met
145 150 155 160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu
165 170 175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile

D

180

185

190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu

195

200

205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala

210

215

220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu

225

230

235

240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile

245

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255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys

260

265

270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly

275

280

285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile

290

295

300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp

305

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315

320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr

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330

335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn

340

345

350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala

355

360

365

DZ

D

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val
370 375 380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp
385 390 395 400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val
405 410 415

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg
420 425 430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro
435 440 445

D2

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val
450 455 460

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp
465 470 475 480

Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr
485 490 495

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn
500 505 510

Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile
515 520 525

Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln
530 535 540

D

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser
545 550 555 560

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe
565 570 575

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val
580 585 590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser
595 600 605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val
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Asp Met Lys
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<212> PRT

<213> Homo sapiens

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Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr Glu Ser Leu
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Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr Leu Lys Met
35 40 45

D

Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg
50 55 60

Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser
65 70 75 80

Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp
85 90 95

Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser
100 105 110

Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser
115 120 125

Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser
130 135 140

Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln
145 150 155 160

Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr
165 170 175

Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr
180 185 190

Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu
195 200 205

Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg
210 215 220

Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr

D2

D

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Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys						
		245		250		255
Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu						
		260		265		270
Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu						
		275		280		285
Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly						
		290		295		300
His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile						
		305		310		315
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Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly						
		325		330		335
Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met						
		340		345		350
His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu						
		355		360		365
Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly						
		370		375		380
His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val						
		385		390		395
						400
Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu						
		405		410		415

D2

D

Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu
420 425 430

Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile
435 440 445

Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly
450 455 460

His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val
465 470 475 480

Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly
485 490 495

D2 Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val
500 505 510

Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp
515 520 525

Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn
530 535 540

Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile
545 550 555 560

Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly
565 570 575

Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys
580 585 590

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<211> 553

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<213> Homo sapiens

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Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys

35 40 45

Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln

50 55 60

Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro Thr Gly Leu

65 70 75 80

Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu

85 90 95

Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr Gln Val Lys

100 105 110

His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser

115 120 125

Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro
130 135 140

Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu
145 150 155 160

Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile
165 170 175

Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys Pro Gly Phe
180 185 190

Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His Arg Ile Asp
195 200 205

Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val Leu Lys Gly
210 215 220

D2

His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile
225 230 235 240

Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser Ala Val Thr
245 250 255

Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly Val Trp Ser
260 265 270

Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr
275 280 285

Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His Thr Leu Tyr
290 295 300

Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu Lys Arg Val

D

305		310		315		320
Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp Ile Glu Thr						
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Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala Val Arg Cys						
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Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr Asp Phe Met						
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Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His Thr Leu Gln						
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Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly Ile His Val						
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Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp Val Glu Thr						
		405		410		415
Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu Thr Ser Gly						
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Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala Asp Ser Thr						
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Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln						
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Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln Phe Asn Lys						
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Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys Leu Trp Asp						
		485		490		495

D2

D

Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu Glu Ser Gly
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Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu
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Val Leu Asp Phe Asp Val Asp Met Lys
545 550

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<213> Homo sapiens

<400> 6

Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser Glu Val
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Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly
35 40 45

Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr
50 55 60

Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln
65 70 75 80

D2

D

Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp
85 90 95

Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro
100 105 110

Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu
115 120 125

Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln
130 135 140

Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg
145 150 155 160

D2

Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg
165 170 175

Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala
180 185 190

Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu
195 200 205

Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys
210 215 220

Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr
225 230 235 240

Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val
245 250 255

D

Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile
260 265 270

Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr
275 280 285

Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys
290 295 300

Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr
305 310 315 320

Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met
325 330 335

D2 Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val
340 345 350

Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr
355 360 365

Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser
370 375 380

Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser
385 390 395 400

Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr
405 410 415

Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu
420 425 430

Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr

D

435

440

445

Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala

450

455

460

Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp

465

470

475

480

Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg

485

490

495

Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg

500

505

510

Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn

515

520

525

D2

Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met

530

535

540

Lys

545

<210> 7

<211> 540

<212> PRT

<213> Homo sapiens

<400> 7

Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu

1

5

10

15

Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu

20

25

30

Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala

35

40

45

Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro

50

55

60

Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro

65

70

75

80

Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr

85

90

95

Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp

100

105

110

D2

Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe

115

120

125

Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp

130

135

140

Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu

145

150

155

160

Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys

165

170

175

Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His

180

185

190

Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val

195

200

205

D

Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly
210 215 220

Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser
225 230 235 240

Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly
245 250 255

Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr
260 265 270

Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His
275 280 285

D2

Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu
290 295 300

Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp
305 310 315 320

Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala
325 330 335

Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr
340 345 350

Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His
355 360 365

Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly
370 375 380

D

Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp
385 390 395 400

Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu
405 410 415

Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala
420 425 430

Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln
435 440 445

Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln
450 455 460

Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys
465 470 475 480

Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu
485 490 495

Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn
500 505 510

Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr
515 520 525

Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys
530 535 540

<210> 8

<211> 589

<212> PRT

D2

D

<213> Homo sapiens

<400> 8

Met Ser Lys Pro Gly Lys Pro Thr Leu Asn His Gly Leu Val Pro Val

1 5 10 15

Asp Leu Lys Ser Ala Lys Glu Pro Leu Pro His Gln Thr Val Met Lys

20 25 30

Ile Phe Ser Ile Ser Ile Ile Ala Gln Gly Leu Pro Phe Cys Arg Arg

35 40 45

Arg Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser

50 55 60

Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly

65 70 75 80

Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala

85 90 95

Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro

100 105 110

Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly

115 120 125

Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro

130 135 140

Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg

145 150 155 160

Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser

D2

D

165

170

175

Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr

180

185

190

Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys

195

200

205

Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile

210

215

220

Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln

225

230

235

240

His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys

245

250

255

D2

Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys

260

265

270

Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp

275

280

285

Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly

290

295

300

Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser

305

310

315

320

Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile

325

330

335

His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His

340

345

350

D

Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp
355 360 365

Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala
370 375 380

Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala
385 390 395 400

Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu
405 410 415

His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp
420 425 430

D2

Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp
435 440 445

Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser
450 455 460

Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn
465 470 475 480

Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu
485 490 495

Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu
500 505 510

Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val
515 520 525

D

Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr
530 535 540

Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser
545 550 555 560

Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu
565 570 575

Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys
580 585

<210> 9

<211> 559

<212> PRT

<213> Homo sapiens

D2

<400> 9

Met Lys Ile Phe Ser Ile Ser Ile Ile Ala Gln Gly Leu Pro Phe Cys
1 5 10 15

Arg Arg Arg Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser
20 25 30

Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr
35 40 45

Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu
50 55 60

Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val
65 70 75 80

D

Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp
85 90 95

Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys
100 105 110

Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe
115 120 125

Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val
130 135 140

Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys
145 150 155 160

Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys
165 170 175

Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys
180 185 190

Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile
195 200 205

Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser
210 215 220

Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln
225 230 235 240

Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys
245 250 255

Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His

D2

D

260

265

270

Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser

275

280

285

Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu

290

295

300

Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His

305

310

315

320

Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg

325

330

335

Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His

340

345

350

D2

Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser

355

360

365

Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr

370

375

380

Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln

385

390

395

400

Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg

405

410

415

Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His

420

425

430

Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser

435

440

445

Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln
450 455 460

Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr
465 470 475 480

Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly
485 490 495

Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu
500 505 510

Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg
515 520 525

Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr
530 535 540

Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys
545 550 555

<210> 10

<211> 540

<212> PRT

<213> Homo sapiens

<400> 10

Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu
1 5 10 15

Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu
20 25 30

D2

D

Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala
35 40 45

Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro
50 55 60

Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro
65 70 75 80

Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr
85 90 95

Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp
100 105 110

Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe
115 120 125

Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp
130 135 140

Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu
145 150 155 160

Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys
165 170 175

Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His
180 185 190

Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val
195 200 205

D2

D

Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly
210 215 220

Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser
225 230 235 240

Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly
245 250 255

Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr
260 265 270

Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His
275 280 285

Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu
290 295 300

D2

Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp
305 310 315 320

Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala
325 330 335

Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr
340 345 350

Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His
355 360 365

Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly
370 375 380

Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp

D

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 11

cgggatccac catggatgat ggatcgatga cacc

34

<210> 12

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

D2

<400> 12

ggaattcctt aagggtatac agcatcaaag tcg

33

<210> 13

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 13

tcacttcatg tccacatcaa agtcc

25

<210> 14

<211> 26

D

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 14

ggtaattaca agttcttggt gaactg

26

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 15

ccctgcaacg tgtgtagaca gg

22

<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 16

ccagtctctg cattccacac ttg

24

D2

D

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 17

ctcagacagg tcaggacatt tgg

23

<210> 18

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 18

ggaattccat gaaaagattg gaccatggtt ctg

33

<210> 19

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 19

D2

D

ggaattcctc acttcatgtc acatcaaagt ccag

34

<210> 20

<211> 1881

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 myc tagged

homo sapiens

<400> 20

DZ

atggagcaaa agctcatttc tgaagaggac ttgaatgaaa tggagcaaaa gctcatttct 60
gaagaggact tgaatgaaat ggagcaaaag ctcatctctg aagaggactt gaatgaaatg 120
gagcaaaagc tcatttctga agaggacttg aatgaaatgg agcaaaagct catttctgaa 180
gaggacttga atgaaatgga gagcttgggc gacctcacca tggagcaaaa gctcatttct 240
gaagaggact tgaattccat gaaaagaaag ttggaccatg gttctgaggt ccgctctttt 300
tctttgggaa agaaaccatg caaagtctca gaatatacaa gtaccactgg gcttgtacca 360
tgttcagcaa caccaacaac ttttggggac ctgagagcag ccaatggcca agggcaacaa 420
cgagcggcaa ttacatctgt ccagccacct acaggcctcc aggaatggct aaaaatgttt 480
cagagctgga gtggaccaga gaaattgctt gctttagatg aactcattga tagttgtgaa 540
ccaacacaag taaaacatat gatgcaagtg atagaacccc agtttcaacg agacttcatt 600
tcattgctcc ctaaagagtt ggcactctat gtgctttcat tcttggaaacc caaagacctg 660
ctacaagcag ctgagacatg tcgctactgg agaattttgg ctgaagacaa ctttctctgg 720
agagagaaat gcaagaaga ggggattgat gaaccattgc acatcaagag aagaaaagta 780
ataaaaccag gtttcataca cagtccatgg aaaagtgcac acatcagaca gcacagaatt 840
gatactaact ggaggcgagg agaactcaaa tctcctaagg tgctgaaagg acatgatgat 900
catgtgatca catgcttaca gttttgtggt aaccgaatag ttagtggttc tgatgacaac 960
actttaaaag tttggtcagc agtcacaggc aatgtctga gaacattagt gggacataca 1020
ggtggagtat ggtcatcaca aatgaggggac aacatcatca ttagtggtac tacagatcgg 1080
acactcaaag tgtggaatgc agagactgga gaatgtatac acaccttata tgggcatact 1140
tccactgtgc gttgtatgca tcttcatgaa aaaagagttg ttagcgggttc tcgagatgcc 1200
actcttaggg tttgggatat tgagacaggc cagtgtttac atgttttgat gggatcatgtt 1260
gcagcagtcg gctgtgttca atatgatggc aggagggttg ttagtgaggc atatgatattt 1320

atggtaaagg tgtgggatcc agagactgaa acctgtctac acacgttgca ggggcatact 1380
 aatagagtct attcattaca gtttgatggt atccatgtgg tgagtggatc tcttgataca 1440
 tccatccgtg tttgggatgt ggagacaggg aattgcattc acacgttaac agggcaccag 1500
 tcgttaacaa gtggaatgga actcaaagac aatattcttg tctctgggaa tgcagattct 1560
 acagttaaaa tctgggatat caaaacagga cagtgtttac aaacattgca aggtcccaac 1620
 aagcatcaga gtgctgtgac ctgtttacag ttcaacaaga actttgtaat taccagctca 1680
 gatgatggaa ctgtaaaact atgggacttg aaaacgggtg aatttattcg aaacctagtc 1740
 acattggaga gtggggggag tgggggagtt gtgtggcgga tcagagcctc aaacacaaaag 1800
 ctgggtgtg cagttgggag tcggaatggg actgaagaaa ccaagctgct ggtgctggac 1860
 tttgatgtgg acatgaagtg a 1881

<210> 21

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 myc tagged
 homo sapien

D2

<400> 21

Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Glu Met Glu Gln
 1 5 10 15

Lys Leu Ile Ser Glu Glu Asp Leu Asn Glu Met Glu Gln Lys Leu Ile
 20 25 30

Ser Glu Glu Asp Leu Asn Glu Met Glu Gln Lys Leu Ile Ser Glu Glu
 35 40 45

Asp Leu Asn Glu Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 50 55 60

Glu Met Glu Ser Leu Gly Asp Leu Thr Met Glu Gln Lys Leu Ile Ser

D

65 70 75 80

Glu Glu Asp Leu Asn Ser Met Lys Arg Lys Leu Asp His Gly Ser Glu
85 90 95

Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr
100 105 110

Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe
115 120 125

Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile
130 135 140

DZ

Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe
145 150 155 160

Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile
165 170 175

Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu
180 185 190

Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala
195 200 205

Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala
210 215 220

Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp
225 230 235 240

Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys
245 250 255

D

Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser
260 265 270

Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu
275 280 285

Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr
290 295 300

Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn
305 310 315 320

D2

Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu
325 330 335

Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile
340 345 350

Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu
355 360 365

Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg
370 375 380

Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala
385 390 395 400

Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu
405 410 415

Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg
420 425 430

Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu
435 440 445

Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr
450 455 460

Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr
465 470 475 480

Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu
485 490 495

Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile
500 505 510

Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys
515 520 525

Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser
530 535 540

Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser
545 550 555 560

Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile
565 570 575

Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp
580 585 590

Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg
595 600 605

Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp

610

615

620

Met Lys

625

<210> 22

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 22

gggtaccacct cattattccc tcgagttctt c

31

<210> 23

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 23

ggaattcctt catgtccaca tcaaagtcc

29

<210> 24

<211> 2010

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: V5HIS tagged

homo sapien

<400> 24

atgtgtgtcc cgagaagcgg tttgatactg agctgcattt gcctttactg tggagttttg 60
ttgccggttc tgctccctaa tcttcctttt ctgacgtgcc tgagcatgtc cacattagaa 120
tctgtgacat acctacctga aaaaggttta tattgtcaga gactgccaaag cagccggaca 180
cacgggggca cagaatcact gaaggggaaa aatacagaaa atatgggttt ctacggcaca 240
ttaaaaatga ttttttacia aatgaaaaga aagtggacc atggttctga ggtccgctct 300
ttttctttgg gaaagaaacc atgcaaagtc tcagaatata caagtaccac tgggcttgta 360
ccatgttcag caacaccaac aacttttggg gacctcagag cagccaatgg ccaagggcaa 420
caacgacgcc gaattacatc tgtccagcca cctacaggcc tccaggaatg gctaaaaatg 480
tttcagagct ggagtggacc agagaaattg cttgctttag atgaactcat tgatagttgt 540
gaaccaacac aagtaaaaca tatgatgcaa gtgatagaac cccagtttca acgagacttc 600
atctcattgc tcctaaaga gttggcactc tatgtgcttt cattcctgga acccaaagac 660
ctgctacaag cagctcagac atgtcgctac tggagaattt tggctgaaga caaccttctc 720
tggagagaga aatgcaaaga agaggggatt gatgaacat tgcacatcaa gagaagaaaa 780
gtaataaaac caggtttcat acacagtcca tggaaaagtg catacatcag acagcacaga 840
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gatcatgtga tcacatgctt acagttttgt ggtaaccgaa tagttagtgg ttctgatgac 960
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gccactctta gggtttggga tattgagaca ggccagtgtt tacatgtttt gatgggtcat 1260
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cagtcgtaa caagtggaat ggaactcaaa gacaatattc ttgtctctgg gaatgcagat 1560
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 aagctggtgt gtgcagttgg gagtcggaat gggactgaag aaaccaagct gctggtgctg 1860
 gactttgatg tggacatgaa ggaattctgc agatatccag cacagtggcg gccgctcgag 1920
 tctagagggc ctttogaagg taagcctatc cctaaccctc tctcgggtct cgattctacg 1980
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<210> 25

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: V5HIS tagged

homo sapien

D2

<400> 25

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr

1 5 10 15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr

20 25 30

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys

35 40 45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr

50 55 60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr

65 70 75 80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser

85 90 95

D

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu
100 105 110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr
115 120 125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg
130 135 140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met
145 150 155 160

D2
Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu
165 170 175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile
180 185 190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu
195 200 205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala
210 215 220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu
225 230 235 240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile
245 250 255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys
260 265 270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly
275 280 285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile
290 295 300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp
305 310 315 320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr
325 330 335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn
340 345 350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala
355 360 365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val
370 375 380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp
385 390 395 400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val
405 410 415

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg
420 425 430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro
435 440 445

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val

D2

D

Ser Arg Gly Pro Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly
645 650 655

Leu Asp Ser Thr Arg Thr Gly His His His His His His
660 665

<210> 26

<211> 2001

<212> DNA

<213> Artificial Sequence

D2

<220>

<223> Description of Artificial Sequence: MYCHIS tagged
homo sapiens

<400> 26

atgtgtgtcc cgagaagcgg tttgatactg agctgcattt gcctttactg tggagttttg 60
ttgccgggtc tgctccctaa tcttcctttt ctgacgtgcc tgagcatgtc cacattagaa 120
tctgtgacat acctacctga aaaaggttta tattgtcaga gactgccaaag cagccggaca 180
cacgggggca cagaatcact gaaggggaaa aatacagaaa atatgggttt ctacggcaca 240
ttaaaaatga ttttttacia aatgaaaaga aagttggacc atggttctga ggtccgctct 300
ttttctttgg gaaagaaacc atgcaaagtc tcagaatata caagtaccac tgggcttcta 360
ccatgttcag caacaccaac aacttttggg gacctcagag cagccaatgg ccaagggcaa 420
caacgacgcc gaattacatc tgtccagcca cctacaggcc tccaggaatg gctaaaaatg 480
tttcagagct ggagtggacc agagaaattg cttgcttttag atgaactcat tgatagttgt 540
gaaccaacac aagtaaaaca tatgatgcaa gtgatagaac cccagtttca acgagacttc 600
atttcattgc tccctaaaga gttggcactc tatgtgcttt cattcctgga acccaaagac 660
ctgctacaag cagctcagac atgtcgctac tggagaattt tggctgaaga caaccttctc 720
tggagagaga aatgcaaaga agaggggatt gatgaacat tgcacatcaa gagaagaaaa 780
gtaataaac caggtttcat acacagtcca tggaaaagtg catacatcag acagcacaga 840
attgatacta actggaggcg aggagaactc aaatctccta aggtgctgaa aggacatgat 900
gatcatgtga tcacatgctt acagttttgt ggtaaccgaa tagttagtgg ttctgatgac 960

aacactttaa aagtttggtc agcagtcaca ggcaaatgtc tgagaacatt agtgggacat 1020
 acaggtggag tatggtcatc acaaatgaga gacaacatca tcattagtgg atctacagat 1080
 cggacactca aagtgtgga tgacagagact ggagaatgta tacacacctt atatgggcat 1140
 acttcactg tgcgttgat gcatcttcat gaaaaagag ttgttagcgg ttctcgagat 1200
 gccactctta gggtttggga tattgagaca ggccagtgtt tacatgtttt gatgggtcat 1260
 gttgcagcag tccgctgtgt tcaatatgat ggcaggaggg ttgttagtgg agcatatgat 1320
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 actaatagag tctattcatt acagttagt ggatccatg tggtagtgg atctcttgat 1440
 acatcaatcc gtgtttggga tgtggagaca ggaattgca ttcacacgtt aacagggcac 1500
 cagtcgttaa caagtggaat ggaactcaaa gacaatattc ttgtctctgg gaatgcagat 1560
 tctacagtta aatctggga tatcaaaaca ggacagtgtt tacaacatt gcaaggtccc 1620
 aacaagcatc agagtgtgt gacctgttta cagttcaaca agaactttgt aattaccagc 1680
 tcagatgatg gaactgtaaa actatgggac ttgaaaacgg gtgaatttat tcgaaaccta 1740
 gtcacattgg agagtggggg gagtggggga gttgtgtggc ggatcagagc ctcaaacaca 1800
 aagctggtgt gtgcagttgg gagtcggaat gggactgaag aaaccaagct gctggtgctg 1860
 gactttgatg tggacatgaa ggaattctgc agatatccag cacagtggcg gccgctcgag 1920
 tctagagggc ccttogaaca aaaactcatc tcagaagagg atctgaatat gcataccggt 1980
 catcatcacc atcaccattg a 2001

DZ

<210> 27

<211> 666

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MYCHIS tagged

homo sapiens

<400> 27

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr

1 5 10 15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr

20 25 30

D

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys
35 40 45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr
50 55 60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr
65 70 75 80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser
85 90 95

D2
Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu
100 105 110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr
115 120 125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg
130 135 140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met
145 150 155 160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu
165 170 175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile
180 185 190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu
195 200 205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala
210 215 220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu
225 230 235 240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile
245 250 255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys
260 265 270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly
275 280 285

DZ

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile
290 295 300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp
305 310 315 320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr
325 330 335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn
340 345 350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala
355 360 365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val
370 375 380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp

D

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val
580 585 590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser
595 600 605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val
610 615 620

Asp Met Lys Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg Pro Leu Glu
625 630 635 640

Ser Arg Gly Pro Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
645 650 655

Met His Thr Gly His His His His His His
660 665

<210> 28

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 28

tcacttcatgtccacatcaaagtcc

25

<210> 29

<211> 27

D

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 29

ggtaattacaaagttcttgttgaactg

27

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 30

ccctgcaacgtgtgtagacagg

22

<210> 31

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 31

ccagtctctgcattccacactttg

24

<210> 32

D2

D

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

DZ

<400> 32

ctcagacaggtcaggacatttgg

23

<210> 28

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 28

tcacttcgatgtccacatcaaagtcc

25

D2
<210> 29

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 29

ggtaattacaaagttcttgttgaactg

27

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 30.

D

ccctgcaacgtgtgtagacagg

22

<210> 31

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

D2
<400> 31

ccagtctctgcattccacactttg

24

<210> 32

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 32

ctcagacaggtcaggacatttgg

23

D